

EXHIBIT B

ClustalW (v1.4) multiple sequence alignment

1. huLGR8-A vs. huLGR8-C

Aligned Length = 754 Gaps = 3
Identities = 681 (90%) Similarities = 0 (0%)

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huLGR8-A   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTIPSCQKGYF   50
huLGR8-C   1 MIVFLVFKHLFSLRLITMFFLLHFIVLINVKDFALTQGSMTIPSCQKGYF   50
*****

huLGR8-A  51 PCGNLTkCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV  100
huLGR8-C  51 PCGNLTkCLPRAFHCDGKDDCGNGADEENCGDTSGWATIFGTVHGNANSV  100
*****

huLGR8-A 101 ALTQECFLKQYPQCCDCKETELECvNGDLKSVPMISNNVTLLSLKKNKIh  150
huLGR8-C 101 ALTQECFLKQYPQCCDCKETELECvNGDLKSVPMISNNVTLLSLKKNKIh  150
*****

huLGR8-A 151 SLpDKVFIKYTKLKKIFLQHNCIRHISRKAffGLCNLQILyLNHNcITTL  200
huLGR8-C 151 SLpDKVFIKYTKLKKIFLQHNCIRHISRKAffGLCNLQIL-----  190
*****

huLGR8-A 201 RpgIFKDLHQLTWLILDDNPITRISQRLFTGLNSLFFLSMVNNYLeALPK  250
huLGR8-C 191 -----ILDDNPITRISQRLFTGLNSLFFLSMVNNYLeALPK  226
*****

huLGR8-A 251 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLFLPRNQIGFVPEKT  300
huLGR8-C 227 QMCAQMPQLNWVDLEGNRIKYLTNSTFLSCDSLTVLDL-----  264
*****

huLGR8-A 301 FSSlKnlGELDLSSNTITeLSPHLfKDLKLLQKLnLSSNPLMyLhKnQfE  350
huLGR8-C 265 -----SSNTITeLSPHLfKDLKLLQKL-----  286
*****

huLGR8-A 351 SLKQLQSLDLERIEIPNINTRMFQPMKnlSHIyFKNFRYCSyAPHVRICM  400
huLGR8-C 287 -----DLERIEIPNINTRMFQPMKnlSHIyFKNFRYCSyAPHVRICM  328
*****

huLGR8-A 401 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRsFIKAENTTh  450
huLGR8-C 329 PLTDGISSFEDLLANNILRIFVWVIAFITCFGNLFVIGMRsFIKAENTTh  378
*****

huLGR8-A 451 AMsIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMeSVQCRLMGF  500
huLGR8-C 379 AMsIKILCCADCLMGVYLFFVGIFDIKYRGQYQKYALLWMeSVQCRLMGF  428
*****

huLGR8-A 501 LAMlStEVSvLLLTyLTLEKFLVIVFPFSNIRPGKRQTSvILICIWMAgF  550
huLGR8-C 429 LAMlStEVSvLLLTyLTLEKFLVIVFPFSNIRPGKRQTSvILICIWMAgF  478
*****

huLGR8-A 551 LIaViPFWNKDYFGNFYgKNGVCfPLYyDQTEDIgSKGYSLGIFLGvNLL  600
huLGR8-C 479 LIaViPFWNKDYFGNFYgKNGVCfPLYyDQTEDIgSKGYSLGIFLGvNLL  528
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huLGR8-A 601 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 650
huLGR8-C 529 AFLIIVFSYITMFCSIQKTALQTTEVRNCFGREVAVANRFFFIVFSDAIC 578
*****

huLGR8-A 651 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 700
huLGR8-C 579 WIPVFVVKILSLFRVEIPDTMTSWIVIFFLPVNSALNPILYTLTTNFFKD 628
*****

huLGR8-A 701 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 750
huLGR8-C 629 KLKQLLHKHQKRSIFKIKKKSLSTSIVWIEDSSSLKLGVLNKITLGDSIM 678
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huLGR8-A 751 KPVS 754
huLGR8-C 679 KPVS 682
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